

AMENDMENTS TO THE CLAIMS

Claims 1-124 (Cancelled)

125. (New) A method of comparing at least one chromosome or part thereof from a cell with a first karyotype with the corresponding chromosome or part thereof from a cell with a second karyotype, the method including the steps of:

(a) randomly amplifying DNA from an isolated chromosome or part of an isolated chromosome, the amplified DNA being depleted of repetitive sequences and/or sequences that are over represented due to the random amplification;

(b) attaching the amplified DNA to a solid substrate;

(c) amplifying DNA from one or more cells with a first karyotype and amplifying DNA from one or more cells with a second karyotype;

(d) labelling the amplified DNA from the one or more cells with a first karyotype with a first label, and labelling the amplified DNA from the one or more cells with a second karyotype with a second label, wherein the first and second labels are detectably different;

(e) hybridizing the amplified and labelled DNA from the one or more cells with a first karyotype to the amplified DNA attached to the solid substrate, and hybridizing the amplified and labelled DNA from the one or more cells with a second karyotype to the amplified DNA attached to the solid substrate; and

(f) comparing the relative amount of first and second labels hybridized to the amplified DNA attached to the solid substrate.

126. (New) A method according to claim 125, wherein the part of an isolated chromosome is a cloned fragment of a chromosome.

127. (New) A method according to claims 125 or 126, wherein the repetitive sequences include Cot-1 sequences, simple repeated DNA, satellite repeats, mini-satellite repeats, chromosome-specific repeats, micro-satellite repeats, repeated genes, sequences derived from transposable elements, elements derived from multiple copies of viruses such as retroviruses, repeats associated with centromeres or telomeres, and repeats associated with heterochromatin.

128. (New) A method according to claim 125, wherein the amplifying of DNA from one or more cells with a first karyotype and the amplifying of DNA from one or more cells with a second karyotype is randomly primed amplification.

129. (New) A method according to claim 125, wherein the amplified DNA from one or more cells with a first karyotype is DNA amplified from 1 to 20 cells.

130. (New) A method according to claim 125, wherein the one or more cells with a first karyotype is an embryonic cell, a foetal cell, a germ cell, a cancerous cell, or a polar body.

131. (New) A method according to claim 125, wherein the method is used to detect a chromosomal abnormality in a cell, for the pre-implantation diagnosis of an embryo or an

oocyte, for the prenatal diagnosis of a foetus for a chromosomal abnormality, or for the determination of karyotype of a cancerous cell.

132. (New) A method according to claim 131, wherein the chromosomal abnormality is selected from the group consisting of an extra or missing individual chromosome, an extra or missing portion of a chromosome, a chromosomal break, a chromosomal rearrangement, a translocation, a dicentric chromosome, an inversion, an insertion, an amplification of a chromosomal region, a deletion, and a point mutation.

133. (New) A nucleic acid attached to a solid substrate, wherein the nucleic acid is derived from an isolated chromosome or part of an isolated chromosome and the nucleic acid is depleted of repetitive sequences.

134. (New) A nucleic acid according to claim 133, wherein the nucleic acid is derived from random amplification of an isolated chromosome or part of an isolated chromosome.

135. (New) A nucleic acid according to claim 133, wherein the part of an isolated chromosome is a cloned fragment of a chromosome.

136. (New) A nucleic acid according to claim 133, wherein the repetitive sequences include Cot-1 sequences, simple repeated DNA, satellite repeats, mini-satellite repeats, chromosome-specific repeats, micro-satellite repeats, repeated genes, sequences derived from

transposable elements, elements derived from multiple copies of viruses such as retroviruses, repeats associated with centromeres or telomeres, and repeats associated with heterochromatin.

137. (New) A nucleic acid according to claim 133, wherein the nucleic acid attached to the substrate is a target for use in comparative genomic hybridisation.

138. (New) An array of nucleic acids, the array including one or more nucleic acids attached to a solid substrate according to claim 133.

139. (New) A method of comparing at least one chromosome or part thereof from a cell with a first karyotype with the corresponding chromosome or part thereof from a cell with a second karyotype, the method including the steps of:

(a) randomly amplifying DNA from an isolated chromosome or part of an isolated chromosome;

(b) attaching the amplified DNA to a solid substrate;

(c) randomly amplifying DNA from 100 or less cells with a first karyotype and randomly amplifying DNA from one or more cells with a second karyotype;

(d) labelling the randomly amplified DNA from the cells with a first karyotype with a first label, and labelling the randomly amplified DNA from the one or more cells with a second karyotype with a second label, wherein the first and second labels are detectably different;

(e) hybridising the amplified and labelled DNA from the cells with a first karyotype to the amplified DNA attached to the solid substrate, and hybridising the amplified and labelled

DNA from the one or more cells with a second karyotype to the amplified DNA attached to the solid substrate; and

(f) comparing the relative amount of first and second labels hybridised to the amplified DNA attached to the solid substrate.

140. (New) A method according to claim 139, wherein the part of an isolated chromosome is a cloned fragment of a chromosome.

141. (New) A method according to claim 139, wherein the repetitive sequences include Cot-1 sequences, simple repeated DNA, satellite repeats, mini-satellite repeats, chromosome-specific repeats, micro-satellite repeats, repeated genes, sequences derived from transposable elements, elements derived from multiple copies of viruses such as retroviruses, repeats associated with centromeres or telomeres, and repeats associated with heterochromatin.

142. (New) A method according to claim 139, wherein the random amplification of DNA from cells with a first karyotype is direct amplification of DNA extracted from the cells.

143. (New) A method according to claim 142, wherein lysis of the cells with a first karyotype and the random amplification of the DNA resulting from the lysis occur in the same tube.

144. (New) A method according to claim 139, wherein the method includes the step of performing a further round of random amplification of the DNA randomly amplified from the cells with a first karyotype and the labelling of the DNA with a first label occurs concurrently with and/or after the further round of random amplification.

145. (New) A method according to claim 139, wherein the one or more cells with a first karyotype is an embryonic cell, a foetal cell, a germ cell, a cancerous cell, or a polar body.

146. (New) A method according to claim 139, wherein the method is used to detect a chromosomal abnormality in a cell, for the pre-implantation diagnosis of an embryo or an oocyte, for the prenatal diagnosis of a foetus for a chromosomal abnormality, or for the determination of karyotype of a cancerous cell.

147. (New) A method according to claim 146, wherein the chromosomal abnormality is selected from the group consisting of an extra or missing individual chromosome, an extra or missing portion of a chromosome, a chromosomal break, a chromosomal rearrangement, a translocation, a dicentric chromosome, an inversion, an insertion, an amplification of a chromosomal region, a deletion, and a point mutation.